

# SEQUENCE LISTING

<110> DE WAARD, Michel  
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 GRUNWALD, Didier  
 SANDOZ, Guillaume

<120> CHIMERIC PROTEIN FOR THE SCREENING OF AGONISTS AND ANTAGONISTS OF  
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 <141> 2005-06-22

<150> PCT/FR03/003860  
 <151> 2003-12-22

<150> FR 02/16576  
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Ser	Ala	Asp	Ser	Tyr	Thr	Ser	Arg	Pro	Ser	Leu	Asp	Ser	Asp	Val	Ser	
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ctg	gag	gag	gac	cgg	gag	agt	gcc	cgg	cga	gaa	gtg	gag	agt	cag	gct	144
Leu	Glu	Glu	Asp	Arg	Glu	Ser	Ala	Arg	Arg	Glu	Val	Glu	Ser	Gln	Ala	
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cag	cag	cag	ctg	gaa	aga	gcc	aag	cac	aaa	cct	gtg	gca	ttt	gct	gtg	192
Gln	Gln	Gln	Leu	Glu	Arg	Ala	Lys	His	Lys	Pro	Val	Ala	Phe	Ala	Val	
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Gln	Gly	Ser	Gly	Val	Asn	Phe	Glu	Ala	Lys	Asp	Phe	Leu	His	Ile	Lys	
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Glu	Lys	Tyr	Ser	Asn	Asp	Trp	Trp	Ile	Gly	Arg	Leu	Val	Lys	Glu	Gly	
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Gly	Asp	Ile	Ala	Phe	Ile	Pro	Ser	Pro	Gln	Arg	Leu	Glu	Ser	Ile	Arg	
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Ser	Asp	Ile	Gly	Asn	Arg	Arg	Ser	Pro	Pro	Pro	Ser	Leu	Ala	Lys	Gln	
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Lys	Gln	Lys	Gln	Ala	Glu	His	Val	Pro	Pro	Tyr	Asp	Val	Val	Pro	Ser	
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Met	Arg	Pro	Val	Val	Leu	Val	Gly	Pro	Ser	Leu	Lys	Gly	Tyr	Glu	Val	
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Thr	Asp	Met	Met	Gln	Lys	Ala	Leu	Phe	Asp	Phe	Leu	Lys	His	Arg	Phe	
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Asp	Gly	Arg	Ile	Ser	Ile	Thr	Arg	Val	Thr	Ala	Asp	Leu	Ser	Leu	Ala	
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Lys	Arg	Ser	Val	Leu	Asn	Asn	Pro	Gly	Lys	Arg	Thr	Ile	Ile	Glu	Arg	
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Ser	Ser	Ala	Arg	Ser	Ser	Ile	Ala	Glu	Val	Gln	Ser	Glu	Ile	Glu	Arg	
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ata	ttc	gag	ctg	gcc	aaa	tcc	ctg	cag	cta	gtg	gtg	ttg	gat	gct	gac	816
Ile	Phe	Glu	Leu	Ala	Lys	Ser	Leu	Gln	Leu	Val	Val	Leu	Asp	Ala	Asp	
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cgc gca ttc ctg aag ctg cgg cgg cag cag cag att gaa cgc gag ctc	1536

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Asn	Gly	Tyr	Met	Glu	Trp	Ile	Ser	Lys	Ala	Glu	Glu	Val	Ile	Leu	Ala		
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Ala	Arg	Ala	Ser	Ile	Lys	Ser	Ala	Lys	Leu	Glu	Asn	Ser	Ser	Phe	Phe		
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cac	aaa	aaa	gag	agg	aga	atg	cgt	ttc	tac	atc	cgt	cgc	atg	gtc	aaa		1824
His	Lys	Lys	Glu	Arg	Arg	Met	Arg	Phe	Tyr	Ile	Arg	Arg	Met	Val	Lys		
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Thr	Gln																
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			20					25					30				
Leu	Glu	Glu	Asp	Arg	Glu	Ser	Ala	Arg	Arg	Glu	Val	Glu	Ser	Gln	Ala		
		35					40					45					
Gln	Gln	Gln	Leu	Glu	Arg	Ala	Lys	His	Lys	Pro	Val	Ala	Phe	Ala	Val		
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Arg Thr Asn Val Ser Tyr Cys Gly Val Leu Asp Glu Glu Cys Pro Val  
65 70 75 80

Gln Gly Ser Gly Val Asn Phe Glu Ala Lys Asp Phe Leu His Ile Lys  
85 90 95

Glu Lys Tyr Ser Asn Asp Trp Trp Ile Gly Arg Leu Val Lys Glu Gly  
100 105 110

Gly Asp Ile Ala Phe Ile Pro Ser Pro Gln Arg Leu Glu Ser Ile Arg  
115 120 125

Leu Lys Gln Glu Gln Lys Ala Arg Arg Ser Gly Asn Pro Ser Ser Leu  
130 135 140

Ser Asp Ile Gly Asn Arg Arg Ser Pro Pro Pro Ser Leu Ala Lys Gln  
145 150 155 160

Lys Gln Lys Gln Ala Glu His Val Pro Pro Tyr Asp Val Val Pro Ser  
165 170 175

Met Arg Pro Val Val Leu Val Gly Pro Ser Leu Lys Gly Tyr Glu Val  
180 185 190

Thr Asp Met Met Gln Lys Ala Leu Phe Asp Phe Leu Lys His Arg Phe  
195 200 205

Asp Gly Arg Ile Ser Ile Thr Arg Val Thr Ala Asp Leu Ser Leu Ala  
210 215 220

Lys Arg Ser Val Leu Asn Asn Pro Gly Lys Arg Thr Ile Ile Glu Arg  
225 230 235 240

Ser Ser Ala Arg Ser Ser Ile Ala Glu Val Gln Ser Glu Ile Glu Arg  
245 250 255

Ile Phe Glu Leu Ala Lys Ser Leu Gln Leu Val Val Leu Asp Ala Asp  
260 265 270

Thr Ile Asn His Pro Ala Gln Leu Ala Lys Thr Ser Leu Ala Pro Ile  
275 280 285

Ile Val Phe Val Lys Val Ser Ser Pro Lys Val Leu Gln Arg Leu Ile  
290 295 300

Arg Ser Arg Gly Lys Ser Gln Met Lys His Leu Thr Val Gln Met Met  
305 310 315 320

Ala Tyr Asp Lys Leu Val Gln Cys Pro Pro Glu Ser Phe Asp Val Ile  
325 330 335

Leu Asp Glu Asn Gln Leu Asp Asp Ala Cys Glu His Leu Ala Glu Tyr  
340 345 350

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355 360 365

Met Leu Gly Pro Pro Ser Ala Ile Pro Gly Leu Gln Asn Gln Gln Leu  
370 375 380

Leu Gly Glu Arg Gly Glu Glu His Ser Pro Leu Glu Arg Asp Ser Leu  
385 390 395 400

Met Pro Ser Asp Glu Ala Ser Glu Ser Ser Arg Gln Ala Trp Thr Gly  
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Ser Ser Gln Arg Ser Ser Arg His Leu Glu Glu Asp Tyr Ala Asp Ala  
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Tyr Gln Asp Leu Tyr Gln Pro His Arg Gln His Thr Ser Gly Leu Pro  
435 440 445

Ser Ala Asn Gly His Asp Pro Gln Asp Arg Leu Leu Ala Gln Asp Ser  
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Glu His Asp His Asn Asp Arg Asn Trp Gln Arg Asn Arg Pro Trp Pro  
465 470 475 480

Lys Asp Ser Tyr Glu Phe Ala Lys Glu Arg Glu Arg Val Glu Asn Arg  
485 490 495

Arg Ala Phe Leu Lys Leu Arg Arg Gln Gln Gln Ile Glu Arg Glu Leu  
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Asn Gly Tyr Met Glu Trp Ile Ser Lys Ala Glu Glu Val Ile Leu Ala

515

520

525

Glu Asp Glu Thr Asp Val Glu Gln Arg His Pro Phe Asp Gly Ala Leu  
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Arg Arg Ala Thr Ile Lys Lys Ser Lys Thr Asp Leu Leu His Pro Glu  
545 550 555 560

Glu Ala Glu Asp Gln Leu Ala Asp Ile Ala Ser Val Gly Ser Pro Phe  
565 570 575

Ala Arg Ala Ser Ile Lys Ser Ala Lys Leu Glu Asn Ser Ser Phe Phe  
580 585 590

His Lys Lys Glu Arg Arg Met Arg Phe Tyr Ile Arg Arg Met Val Lys  
595 600 605

Thr Gln  
610